

**Appendix II: Clean copy of claims as pending upon entry of amendment**

1. A method for the biological production of polyhydroxyalkanoate containing 3-hydroxyhexanoate comprising growing a transgenic organism selected from the group consisting of a transgenic bacterium and a transgenic plant having at least one bacterial transgene encoding an enzyme selected from the group consisting of a PHA polymerase incorporating C<sub>6</sub> substrates and a D-specific enoyl-CoA hydratase, integrated into the chromosome, wherein production of polyhydroxybutyrate-polyhydroxyvalerate containing 3-hydroxyhexanoate by the transgenic organism occurs.
2. The method of claim 1 wherein the organism is a plant.
3. The method of claim 2 wherein the organism is a plant selected from the group consisting of an oil crop plant and a starch accumulating plant.
4. The method of claim 3 wherein the plant is selected from the group consisting of *Brassica*, sunflower, soybean, corn, safflower, flax, palm, coconut, potato, tapioca, cassava, alfalfa, grass, and tobacco.
5. The method of claim 1 wherein the organism is a bacterium selected from the group consisting of *Escherichia*, *Klebsiella*, *Ralstonia*, *Alcaligenes*, *Pseudomonas*, and *Azotobacter*.
6. The method of claim 1 wherein the transgene encodes a PHA polymerase incorporating C<sub>6</sub> substrates.
7. The method of claim 6 wherein the polymerase is from *Aeromonas caviae*, *Comamonas testosteroni*, *Thiocapsia pfenigii*, *Chromatium vinosum*, *Bacillus cereus*, *Nocardia carolina*,

*Nocardia salmonicolor*, *Rhodococcus ruber*, *Rhodococcus rhodocrous*, and *Rhodospirillum rubrum*.

8. The method of claim 1 wherein the organism directs metabolites to production of 3-hydroxyhexanoyl-CoA.
9. The method of claim 8 wherein the transgene encodes a D-specific enoyl-CoA hydratase gene.
10. The method of 9 wherein the hydratase gene is isolated from a bacterium selected from the group consisting of *R. eutropha*, *Klebsiella aerogenes*, *P. putida*, and *Aeromonas caviae*.
11. The method of claim 8 wherein the organism has the genes encoding the enzymes in a butyrate fermentation pathway.
12. The method of claim 11 wherein the enzymes in the butyrate fermentation pathway are from *Clostridium acetobutylicum* or *Thermoanaerobacterium thermosaccharolyticum*.
13. The method of claim 11 wherein the organism converts butyrate to butyryl CoA or butyryl CoA to crotonyl CoA.
14. The method of claim 11 wherein the organism expresses a broad range reductase that is active on C<sub>6</sub> substrates.
15. The method of claim 11 wherein the organism expresses a polymerase that accepts 3-hydroxyhexanoyl CoA.
16. The method of claim 11 wherein the organism expresses a thiolase accepting acetoacetyl CoA.

17. The method of claim 11 wherein the organism expresses an enzyme selected from the group consisting of thiolases specific for 3-ketohexanoyl CoA, reductase active on 3-ketohexanoyl CoA, and 3-hydroxyhexanoyl CoA.
18. The method of claim 8 wherein the organism expresses one or more fatty acid biosynthetic enzymes.
19. The method of claim 18 wherein the fatty acid biosynthetic enzymes are enzymes converting acyl ACP to acyl CoA.
20. The method of claim 19 where the enzymes are selected from the group consisting of ACP-CoA transacylase, acyl ACP thioesterase, and acyl CoA synthase.
21. The method of claim 20 wherein the enzymes are acyl ACP thioesterase and acyl CoA synthase.
22. The method of claim 18 wherein the enzymes are from *E. coli*.
23. The method of claim 8 wherein the organism expresses one or more enzymes forming a fatty acid oxidation complex.
24. The method of claim 23 wherein the one or more enzymes are selected from the group consisting of enzymes epimerizing S-3 hydroxyhexanoyl CoA and enzymes reducing 3-ketohexanoyl CoA.
25. The method of claim 24 wherein the enzymes are from *Nocardia salmonicolor*.
26. The method of claim 24 wherein the enzymes epimerizing S-3 hydroxyhexanoyl CoA are from the *Pseudomonas putida* FaoAB complex.

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AMENDMENT AND RESPONSE TO OFFICE ACTION

27. The method of claim 23 wherein the organism accumulates 3-ketohexanoyl CoA due to a lack of a thiolase.

31. A transgenic bacterium or plant for use in any of the methods of claims 1-27.

32. The transgenic bacterium of claim 31.

33. The transgenic plant of claim 31 wherein the plant is a higher order plant.

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